

Towards An Epidemiological Source Account For Human Campylobacteriosis Of Animal Origin

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In order to implement effective preventive measures against human campylobacteriosis, the relative significance of various possible infection sources needs to be understood. As *C. jejuni* has been shown to express insufficient host specificity for the development of a source account, a new molecular-epidemiological method focusing on the occurrence of identical genotypes among sources was developed.

In the presented study, band patterns generated by fluorescent Amplified Fragment Length Polymorphism (AFLP) of 227 *C. jejuni* isolates from human, poultry, cattle and pets were compared. With Unweighted Pair Group Method with Arithmetic mean (UPGMA) clustering, 136 different phena were identified. The phena were classified into different phenon types according to the different sources that grouped together. The observed frequency of these phenon types revealed important information for the assessment of epidemiological significance of the different sources. Evidence of considerable inter-mingling among sources was obtained, whereas several apparently stable clones were also identified: some strains were shown to remain unchanged over time and unaffected by the passage through different hosts. These stable strains are an important indicator of the significance of contact between the hosts and their importance for human infection can be assessed.

The new insight gained with this approach provides new input towards the development of a source account based on a stochastic exposure model to weight human exposure by the different transmission pathways.